

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 59 Seconds
(without alignments)
1145.669 Million cell updates/sec

Title: US-10-643-836-297
Perfect score: 703
Sequence: 1 MEGAGAYGAGKAGAPDPYTL.....GEPHACTPCTESTEGCPGP 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: 1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
| 1 | 577 | 82.1 | 234 1 | SNGL_HUMAN |
| 2 | 550 | 78.2 | 234 1 | SNGL_MOUSE |
| 3 | 547 | 77.8 | 234 1 | SNGL_RAT |
| 4 | 500 | 71.1 | 231 2 | QBRW67 |
| 5 | 362 | 51.5 | 229 1 | SN33_MOUSE |
| 6 | 353 | 50.2 | 229 1 | SN33_HUMAN |
| 7 | 306 | 43.5 | 219 2 | Q6DIE7 |
| 8 | 304 | 43.2 | 217 2 | Q6AZR4 |
| 9 | 296 | 42.1 | 224 1 | SN32_HUMAN |
| 10 | 289.5 | 41.2 | 224 2 | Q7QHR6 |
| 11 | 287 | 40.8 | 145 2 | Q9V6U3 |
| 12 | 286 | 40.7 | 241 1 | Q9V6U3 |
| 13 | 282 | 40.1 | 234 1 | SN32_RAT |
| 14 | 274 | 39.0 | 224 1 | SN32_MOUSE |
| 15 | 274 | 39.0 | 224 2 | Q9CZ25 |
| 16 | 274 | 39.0 | 224 2 | Q9XK83 |
| 17 | 211 | 30.0 | 191 2 | Q6S9S7 |
| 18 | 192 | 27.3 | 247 1 | SN31_CAEEL |
| 19 | 170 | 24.0 | 233 1 | SN34_MOUSE |
| 20 | 169 | 24.0 | 234 1 | SN34_HUMAN |
| 21 | 167.5 | 23.8 | 236 2 | Q6R6S8 |
| 22 | 85 | 12.1 | 626 2 | Q9NRM1 |
| 23 | 84.5 | 12.0 | 235 2 | Q6PEU1 |
| 24 | 82.5 | 11.7 | 202 2 | Q6S3G7 |
| 25 | 82 | 11.7 | 462 2 | Q9NRM3 |
| 26 | 82 | 11.7 | 907 2 | Q44359 |
| 27 | 81.5 | 11.6 | 161 2 | Q92KJ9 |
| 28 | 80 | 11.4 | 468 1 | PTM8_BACHD |
| 29 | 79.5 | 11.3 | 538 2 | Q6R4H5 |
| 30 | 78 | 11.1 | 392 1 | GCST_CHICK |
| 31 | 77.5 | 11.0 | 650 2 | Q6LKE4 |

| | | | | | | |
|----|------|------|-----|---|------------|------------------------|
| 32 | 76 | 10.8 | 251 | 2 | Q7ZWV8 | Q7ZWV8 xenopus lae |
| 33 | 76 | 10.8 | 288 | 2 | Q6ZM74 | Q6ZM74 brachydanio |
| 34 | 76 | 10.8 | 439 | 2 | Q731J4 | Q731J4 bacillus ce |
| 35 | 76 | 10.8 | 519 | 2 | Q7NFM8 | Q7NFM8 glieobacter |
| 36 | 75.5 | 10.7 | 232 | 2 | Q6TIG1 | Q6TIG1 brachydanio |
| 37 | 75.5 | 10.7 | 348 | 1 | Y479_MYCTU | Y479_MYCTU mycobacteri |
| 38 | 75.5 | 10.7 | 348 | 1 | Y489_MYCBO | Y489_MYCBO mycobacteri |
| 39 | 75.5 | 10.7 | 460 | 2 | Q6P2F0 | Q6P2F0 homo sapien |
| 40 | 75.5 | 10.7 | 530 | 1 | MATP_HUMAN | MATP_HUMAN homo sapien |
| 41 | 75 | 10.7 | 249 | 2 | Q94614 | Q94614 oryza sativ |
| 42 | 75 | 10.7 | 249 | 2 | Q7G6Z4 | Q7G6Z4 oryza sativ |
| 43 | 75 | 10.7 | 439 | 2 | Q635H8 | Q635H8 bacillus ce |
| 44 | 75 | 10.7 | 439 | 2 | Q818Y3 | Q818Y3 bacillus ce |
| 45 | 75 | 10.7 | 439 | 2 | Q81MC4 | Q81MC4 bacillus th |
| 46 | 75 | 10.7 | 439 | 2 | Q6HE62 | Q6HE62 bacillus th |
| 47 | 75 | 10.7 | 667 | 2 | Q8VUH1 | Q8VUH1 streptococc |
| 48 | 75 | 10.7 | 760 | 2 | Q6BLQ5 | Q6BLQ5 debaryomyce |
| 49 | 74.5 | 10.6 | 533 | 2 | Q73FP3 | Q73FP3 bacillus ce |
| 50 | 74.5 | 10.6 | 533 | 2 | Q81VY5 | Q81VY5 bacillus an |

ALIGNMENTS

RESULT 1
ID SNGL_HUMAN STANDARD: PRT: 234 AA.
AC 043759; 043757; 043758; 096J56; 09UG24;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synapcogrytin-1.
GN Name=SYNGR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP MEDLINE=98430994; PubMed=9760194;
RA Kedar D., Pan H.-O., Seroussi B., Fransson I., Guilbaud C.,
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumaniski J.P.,
RA Characterization of the human synapcogrytin gene family." ;
Hum. Genet. 103:131-141(1998).
[2]
RP MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baggeley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Dham P.D., Dockree C., Dodsorth S.J., Durbin R.M., Ellington A.C.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.P., Levergha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Washiegh-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay C.N., Mcclaren S., McMurtry A.A., Milne S.A., Northmore B.J.C.T.,
RA Odell J., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,
RA Scott C.E., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon I., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Winton S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shinnar A., Shibuya K., Yoshizaki Y., Aoki N., Mituyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Pang F., Fu Y., Hu P., Dha A., Kenon S., Lai H.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang Q., Chisoso S., Murray J., Miller N., Mink P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawking J.,
RA Hinde K., Kemp K., Latreille P., Layman D., Ozereky P., Rohlfing T.,
RA Schaepe P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Kott I., Bedell J.A., Hillier L.W., Maris E., Waterson R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McCormick H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Badelmann L., Kim U.J., Shizuya H., Simon M.I., Dunanek J.P.,
RA Peyraud M., Kedra D., Serousai E., Franconi I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliakou Y., Wright H.,
RA "The DNA sequence of human chromosome 22."
RA Nature 402:489-495[1999].
RA [3]
RA SEQUENCE FROM N.A. (ISOFORM 1B).
RA TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marzina K., Farmer A.A., Kudin G.M., Hong L.,
RA Stepien M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson A.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.R., Gunaratne P.H.,
RA Richards S., Morley P.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Heltou E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Sutterich A., Schin J.B., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA -1- SUBCELLULAR LOCATION: Integral membrane protein.
RA -1- ALTERNATIVE PRODUCTS:
RA Event=Alternative splicing; Named isoforms=3;
RA Name=1A;
RA IsoId=O43759-1; Sequence=Displayed;
RA Name=1B;
RA IsoId=O43759-2; Sequence=VSP_006332;
RA Name=1C;
RA IsoId=O43759-3; Sequence=VSP_006331, VSP_006332;
RA -1- SIMILARITY: Belongs to the synapocystin family.
RA -----
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RA or send an email to license@ebi.ac.uk).
RA -----
RA EMBL, AJ002305; CAA05322.1; -
RA EMBL, AJ002304; CAA05321.1; -
RA EMBL, AJ002303; CAA05320.1; -
RA EMBL, AL002326; CAA18451.1; -
RA EMBL, AL002326; CAA18452.1; -
RA EMBL, AL002326; CAA18453.1; -
RA EMBL, BC000731; AAH00731.1; -
RA Genbank, HGNC:11498; SYNGR1.
RA H-invDB, HIX0016490; -
RA MIM, 603925; -
RA GO, GO:0005887; C:Integral to plasma membrane; TAS.
RA InterPro, IPR008253; Marvel.

| | |
|--|--|
| KM | pfam; Pf01284; MARVEL, 1. |
| Dn | Alternative splicing; Synapse; Transmembrane. |
| FT | TRANSMEM 24 44 Potential. |
| FT | TRANSMEM 72 92 Potential. |
| FT | TRANSMEM 104 124 Potential. |
| FT | TRANSMEM 149 169 Potential. |
| FT | VARSPLIC 1 33 MEGAYAGAKGAGAFDPYTLVROPHITLARVVSW -> MLTL EFGLEBDPSMGISWQTGRSWMSPRGCE (in isoform IC). |
| FT | |
| FT | |
| FT | VARSPLIC 162 234 /Prtid=VSP_006331. ACGVLAIFQRVGADSAALFSQDYMDSQSSMEPYAPVEP NTGDVPAGMGCTQQPNPTEDTEBQGYOSOOY -> SLTAA LAVRRFROLSFOBEYSTLPFPASAO P (in Isoform IB and isoform IC). |
| FT | |
| FT | CONFLICT 203 203 Missing (In Ref. 2). |
| SQ | SEQUENCE 234 AA; 25570 MW; 8B015CBBD461E12 CRC64; |
| Query March | 82.1%; Score 577; DB 1; Length 234; |
| Blast Local Similarity | 99.1%; Pred. No. 1,7e-46; |
| Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| Dy | 1 MEGGAYAGKAGAGAFDDPYTLVRQPHITLRVSVMLFSIVTFGSIVNEGYLNASSSGBOFCI 60 1 MEGGAYAGKAGAGAFDDPYTLVRQPHITLRVSVMLFSIVTFGSIVNEGYLNASSSGEBECFI 60 |
| Dz | 61 YNRPNAICSYGVANGVTAFETCLLYLTLDVDYPPOISSVMORKKVLSDIGVS 112 61 YNRNPNCASYGVANGVTAFETCLLYLTLDVDYPPOISSVMORKKAVALSDIGVS 112 |
| <hr/> | |
| RESULT 2 | |
| SNGI MOUSE | |
| ID | SNGI_MOUSE STANDARD; Prt; 234 AA. |
| AC | O55100; O9DCB0; |
| DT | 30-MAY-2000 (Rel. 39, Created) |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) |
| DE | Synapcogrylin-1. |
| GN | Name=Sngri1; |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Sciuromathi; Euteleostomi; |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| CX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. (ISOFORM IB). |
| RX | MEDLINE=98430994; PubMed=9760194; Kedra D., Pan H.-Q., Seroushi E., Fransson I., Guilbad C., Collins J.B., Dunham I., Blennow E., Roe B.A., Piehl F., Dunnanski U.F.; "Characterization of the human synapcogrylin gene family."; Hum. Genet. 103:131-141(1998). [2] |
| RP | SEQUENCE FROM N.A. (ISOFORM IA AND IB). |
| RC | STRAIN=C57BL/6J; TISSUE=Brain. |
| RX | MEDLINE=22354683; PubMed=1246685; DOI=10.1038/nature01286; Okazaki Y., Furuno M., Kasekawa T., Adachi J., Bono H., Kondo S., Nakai I., Osato N., Saio R., Suzuki H., Yamanaoka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderici R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsumura H., Batalov S., Beisel K.W., Blake J.A., Brad T.D., Brusic V., Chochoja C., Corbett L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gisbi C., Godzik A., Gough J., Grimmond S., Gusnetich S., Hirokawa N., Jackson I.J., Jarvis E.D., Karai A., Kawaji H., Kawasaki Y., Kedizertski R.M., King B.L., Konagaya A., Kutrochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H., Nagashima T., Nunata K., Okido T., Pavan W.J., Petosa G., Petrovskiy N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., |

RA Varado R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carrini P., Hayatsu N.,
 RA Hirozane-Klehlhwa T., Kono H., Nakamura N., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawel J., Alzawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imocani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shingawa A.,
 RA Yasumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1A;
 CC IsoId=055100-1; Sequence=Displayed;
 CC Name=1B;
 CC IsoId=055100-2; Sequence=VSP_006333;
 CC -1- SIMILARITY: Belongs to the synapocyrin family.
 CC -----
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 CC -----
 CC EMBL: AJ002306; CA05323.1; -
 DR EMBL: AK002972; BAB22487.1; -
 DR EMBL: AK010442; BAB26943.1; -
 DR MGI: MGI:1328323; Syngri.
 DR InterPro: IPR008253; Marvel.
 DR Pfam: PF01284; MARVEL; 1.
 DR Alternative splicing; Synapse; Transmembrane.
 FT TRANSMEM 24 92 Potential.
 FT TRANSMEM 72 92 Potential.
 FT TRANSMEM 104 124 Potential.
 FT TRANSMEM 149 169 Potential.
 FT VASPLC 162 234 ACQVALAFKRYQIGADSLFSDQYNDPSDSSMPYAPYEP
 SAGSDPAGMGTYOHFANPADEPQGYQGYQ -> SLTRA
 LAVRRPKELTFOEYVTLFPASAP (in isoform
 1B).
 FT FTId=VSP_006333.
 SQ SEQUENCE 234 AA; 25653 MW; 0956602IDP3E809A CRC64;
 Query Match 78.2%; Score 550; DB 1; Length 234;
 Best Local Similarity 93.8%; Pred. No. 6.1e-44;
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNEGYLNSASBEGQFCI 60
 DB 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNEGYLNSASBEGQFCI 60
 QY 61 YNRNPACSGYVAVGLAFITCLLYALDVYFPQISSVDRKKAVALSDIGVS 112
 DB 61 YNRNPACSGYVAVGLAFITCLLYALDVYFPQISSVDRKKAVALSDIGVS 112
 RESULT 3
 SNGI_RAT STANDARD; PRT; 234 AA.
 AC 062876;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Synapocyrin-1 (p29).
 GN Name=Syngri;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96134029; PubMed=8557746; DOI=10.1093/jcb.131.6.1801;
 RX Stenius K., Jantz R., Suedhof T.C., Jahn R.;
 RT "Structure of synapocyrin (p29) defines novel synaptic vesicle
 protein."
 RL J. Cell Biol. 131:1801-1809 (1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Nervous system.
 CC -1- SIMILARITY: Belongs to the synapocyrin family.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U39549; AAB17890.1; -
 DR RGD; 3801; Syngri.
 DR InterPro: IPR008253; Marvel.
 DR Pfam: PF01284; MARVEL; 1.
 DR Synapse; Transmembrane.
 FT TRANSMEM 24 44 Potential.
 FT TRANSMEM 72 92 Potential.
 FT TRANSMEM 105 125 Potential.
 FT TRANSMEM 149 169 Potential.
 SQ SEQUENCE 234 AA; 25669 MW; B3038B64C49F31E1 CRC64;
 Query Match 77.8%; Score 547; DB 1; Length 234;
 Best Local Similarity 92.9%; Pred. No. 1.2e-43;
 Matches 104; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNEGYLNSASBEGQFCI 60
 DB 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNEGYLNSASBEGQFCI 60
 QY 61 YNRNPACSGYVAVGLAFITCLLYALDVYFPQISSVDRKKAVALSDIGVS 112
 DB 61 YNRNPACSGYVAVGLAFITCLLYALDVYFPQISSVDRKKAVALSDIGVS 112
 RESULT 4
 Q8UM67 PRELIMINARY; PRT; 231 AA.
 AC 08UM67;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE P7D11.
 GN Name=P7D11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21643879; PubMed=11784032; DOI=10.1006/dbio.2001.0428;
 RA Shibata M., Itoh M., Ohmori S., Shinga J., Taira M.;
 RT "Systematic screening and expression analysis of the head organizer
 genes in Xenopus embryos."
 RL Dev. Biol. 239:241-256 (2001).
 DR EMBL: AB072005; BAB79596.1; -
 DR GO: GO:0016020; C:membrane; IEA.
 DR Pfam: PF01284; MARVEL; 1.
 SQ SEQUENCE 231 AA; 25535 MW; 03962P903EEB3P14 CRC64;

Query Match 71.1%; Score 500; DB 2; Length 231;
 Best Local Similarity 81.2%; Pred. No. 3.3e-39;
 Matches 91; Conservative 13; Mismatches 8; Indels 0; Gaps 0;